



SEQUENCE LISTING

<110> Yoshida, Roberta
Kootstra, Anna

<120> Phenylalanine Ammonia Lyase Polypeptide and
Polynucleotide Sequences and Methods of Obtaining and
Using Same

<130> 29479/500NSCA

<140> US 09/939,408

<141> 2001-08-24

<150> US 09/624,693

<151> 2000-07-24

<150> PCT/US01/23270

<151> 2001-07-24

<160> 30

<170> PatentIn Ver. 2.0

<210> 1

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description o
primer QLI 61

<400> 1

qacqqatcca ctatqqcbcc btcsqtsqac tcqat

35

<210> 2

<211> 33

<212> RNA

8213 Artificial Sequence

-220-

<221> modified_base
<222> (13)
<223> n = (a or c or g or t/u) or (unknown or other)
<223> Description of Artificial Sequence: Synthetic
Primer OLI 63

<400> 2
gacgaattct tangccatca tcttsacsag gac

33

<210> 3
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (24, 25, 29, 30, 34, 35)
<223> n = i or inosine

<223> Description of Artificial Sequence: Synthetic
Primer AAP

<400> 3
ggccacgcgt cgactagtagc gggnnnnnn gggnnng

36

<210> 4
<211> 33
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer GSP2

<400> 4
cgcgaattca gaatgcctc gtcgtccttg acc

33

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer AUAP

<400> 5

ggccacgcgt cgactagtag

20

<210> 6

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer GSP4

<400> 6

ccggaaattcc gacgagccgg aaaggagcgt gcg

33

<210> 7

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer AP

<400> 7

ggccacgcgt cgactagtagac tttttttttt tttttttt

37

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

Primer GSP5

<400> 8
ggtcaaggac gacgaggggca ttct

24

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer GSP6

<400> 9
ccgggatcca ttagatgcacgc ctactcgact ctctcgct

38

<210> 10
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 77

<400> 10
atcgaattcc actctaaccg gtcactagca ctcgct

36

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 78

<400> 11
atcggatccc acgacacgac gtcgaaaagc tggct

36

<210> 12
<211> 2419
<212> DNA
<213> Rhodotorula graminis

<220>
<221> CDS
<222> (37) .. (2196)

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<221> modified_base
<222> (494)
<223> Other information: y = t or c

<220>
<221> unsure
<222> (493) .. (495)
<223> Other information: Xaa = Val or Ala

<400> 12
ctcctgcctc actctaaccg gtcactagca ctgcgc atg gcc cct tcc ttg gac 54
Met Ala Pro Ser Leu Asp
1 5

tcg ctc gcc acc acg ctc gcc aac ggc ttt acc aac ggc tcg cac gcc 102
Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe Thr Asn Gly Ser His Ala
10 15 20

gct ccg acc aag tcg gct gcg ggc ccc act tcg gct ctc cgc cgc acg 150
Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr Ser Ala Leu Arg Arg Thr
25 30 35

ccc ggc ctc gat ggc cac gcc gcg cac cag tcg cag ctc gag atc gtg 198
Pro Gly Leu Asp Gly His Ala Ala His Gln Ser Gln Leu Glu Ile Val
40 45 50

cag gag ctc ctc agc gac ccc acc gac gac gtc gtc gag ctc agc ggg Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp Val Val Glu Leu Ser Gly	246
55 60 65 70	
 tac agc ctc acc gtc cgt gac gtt gtc ggc gcc gcc cgc aag ggg cgc Tyr Ser Leu Thr Val Arg Asp Val Val Gly Ala Ala Arg Lys Gly Arg	294
75 80 85	
 agg gtc cgc gtc cag aac gac gac gag atc cgc gca cgc gtc gac aag Arg Val Arg Val Gln Asn Asp Asp Glu Ile Arg Ala Arg Val Asp Lys	342
90 95 100	
 agc gtc gac ttc ctc aag gcc cag ctt cag aac tcg gtc tac gga gtc Ser Val Asp Phe Leu Lys Ala Gln Leu Gln Asn Ser Val Tyr Gly Val	390
105 110 115	
 acc acg ggt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc Thr Thr Gly Phe Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val	438
120 125 130	
 agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro	486
135 140 145 150	
 acg tcc gyc tcg tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu	534
155 160 165	
 ccg ctc gag gtc cgc ggc gcc atg gtc atc cgc gtc aac tcg ctc Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu	582
170 175 180	
 acg cgt ggc cac tcg gcc cgc ctc gtc gtc ctt gag gcg ctc acc Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr	630
185 190 195	
 aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc ggc tcc Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser	678
200 205 210	
 atc tcg gcg tcg ggc gac ctc agc ccc atc gtc ccc ctc cgc ggc tcc Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala	726
215 220 225 230	

atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc			774
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr			
235	240	245	
gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag			822
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu			
250	255	260	
gca gtc gtc ctc ggc ccg aag gag ggt ctc ggt ctg gtc aac gga acg			870
Ala Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr			
265	270	275	
gcc gtc tcc gcc tcg atg gcg acc ctc agt ctg cac gac tcg cac atg			918
Ala Val Ser Ala Ser Met Ala Thr Leu Ser Leu His Asp Ser His Met			
280	285	290	
ctc tcg ctc ctc tcg cag gcc ttg acg gct ctc acg gtg gag gcc atg			966
Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met			
295	300	305	310
gtc ggc cag cag ggc tcg ttc gcg ccg ttc atc cac gac gtc tgc cgc			1014
Val Gly Gln Gln Gly Ser Phe Ala Pro Phe Ile His Asp Val Cys Arg			
315	320	325	
ccg cac ccc ggc cag gtc gag gtc gcg cgc aac atc cgc acg ctc ctt			1062
Pro His Pro Gly Gln Val Glu Val Ala Arg Asn Ile Arg Thr Leu Leu			
330	335	340	
tcc ggc tcg tcg ttt gcc gtt gag cac gag gag gtc aag gtc aag			1110
Ser Gly Ser Ser Phe Ala Val Glu His Glu Glu Glu Val Lys Val Lys			
345	350	355	
gac gac gag ggc att ctt cgc cag gac cgc tac ccg ctc cgc acg tcg			1158
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser			
360	365	370	
cct cag ttc ctc ggc ccg ctc gtg gag gac atg atg cac gcc tac tcg			1206
Pro Gln Phe Leu Gly Pro Leu Val Glu Asp Met Met His Ala Tyr Ser			
375	380	385	390

act ctc tcg ctc gag aac aac acg acg acc gac aac ccg ctc ctc gac			1254
Thr Leu Ser Leu Glu Asn Asn Thr Thr Asp Asn Pro Leu Leu Asp			
395	400	405	
gtc gag aac aag cag acc ggc cac ggc aac ttc cag gcg tcg gct			1302
Val Glu Asn Lys Gln Thr Ala His Gly Gly Asn Phe Gln Ala Ser Ala			
410	415	420	
gtc tcg att tcg atg gag aag acc agg ctc gca ctc gcc ctc atc ggc			1350
Val Ser Ile Ser Met Glu Lys Thr Arg Leu Ala Leu Ala Ile Gly			
425	430	435	
aag ctc aac ttc acg cag tgc acc gag ttg ctc aac gct gcc atg aac			1398
Lys Leu Asn Phe Thr Gln Cys Thr Glu Leu Leu Asn Ala Ala Met Asn			
440	445	450	
cgc ggc ctg cct tcg tgc ctc gct gcc gag gac ccg tcg ctc aac tat			1446
Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Asn Tyr			
455	460	465	470
cac ggc aag ggc ttg gac att cac atc gct gct tac gct tcg gag ctc			1494
His Gly Lys Gly Leu Asp Ile His Ile Ala Ala Tyr Ala Ser Glu Leu			
475	480	485	
ggc cac ctt gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg			1542
Gly His Leu Ala Asn Pro Val Thr Phe Val Gln Pro Ala Glu Met			
490	495	500	
ggc aac cag gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act			1590
Gly Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr			
505	510	515	
gcc gag gcc aac gac gtc ctt tct ctc ctt ctc gcc tcg cac ctg tac			1638
Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Ser His Leu Tyr			
520	525	530	
tgc acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag			1686
Cys Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys			
535	540	545	550
aag cag ttc gac ccg ctt ctc ccg act ctc ctc cag cag cac ctc ggc			1734
Lys Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly			
555	560	565	

act ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc	570	575	580	1782
Thr Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu				
aac aag cgt ctc gag cag acg acg tac gac ctc gag ccg cgc tgg	585	590	595	1830
Asn Lys Arg Leu Glu Gln Thr Thr Tyr Asp Leu Glu Pro Arg Trp				
cac gac gcc ttc tcg tac gcg acc ggc acc gtc gtc gag ctc ctc tcg	600	605	610	1878
His Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser				
tcc tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag	615	620	625	1926
Ser Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys				
gtt gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac	635	640	645	1974
Val Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn				
cgc ttc tgg cag acg ccg tct tcg cag gcg ccg gcg cac gca tac ctc	650	655	660	2022
Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu				
tcg ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc ggc	665	670	675	2070
Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly				
gtg cag gcg cgc cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg	680	685	690	2118
Val Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr				
atc ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc	695	700	705	2166
Ile Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg				
atc aac cac gtc ctc gtc aag atg ctc gcg taaggcccgaa gcaaggctcg	715	720		2216
Ile Asn His Val Leu Val Lys Met Leu Ala				
cctagacgcc cgccctcaccc caagaccaggc tttcgacgt cgtgtcgtgc caagaacgga	2276			

ctttcctcca tacacatgtc gccttactct ctgcggta tcacgtctc cagtttttc 2336
gtatcccgcg tctctcggtc gtcagtagac gtgtatagag cctggaatgg attgcaagtc 2396
ttcgagttca aaaaaaaaaaaa aaa

2419

<210> 13
<211> 720
<212> PRT
<213> Rhodotorula graminis

<220>
<221> unsure
<222> (153)
<223> Other information: Xaa = Val or Ala

<400> 13
Met Ala Pro Ser Leu Asp Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe
1 5 10 15

Thr Asn Gly Ser His Ala Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr
20 25 30

Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln
35 40 45

Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp
50 55 60

Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly
65 70 75 80

Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile
85 90 95

Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln
100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Val Ser Leu Gln Lys Ala Leu Ile Glu His Gln
130 135 140

Leu Cys Gly Val Thr Pro Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg
145 150 155 160

Gly Leu Glu Asn Thr Leu Pro Leu Glu Val Val Arg Gly Ala Met Val
165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Arg Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Ser Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
210 215 220

Ser Tyr Ile Ala Gly Ala Ile Thr Gly His Pro Asp Val Lys Val His
225 230 235 240

Val Leu His Glu Gly Thr Glu Lys Ile Met Phe Ala Arg Glu Ala Ile
245 250 255

Ser Leu Phe Gly Leu Glu Ala Val Val Leu Gly Pro Lys Glu Gly Leu
260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
275 280 285

Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
305 310 315 320

Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
325 330 335

Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
340 345 350

Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

Tyr Pro Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Leu Val Glu Asp
370 375 380

Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn Thr Thr Thr
385 390 395 400

Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala His Gly Gly
405 410 415

Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys Thr Arg Leu
420 425 430

Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys Thr Glu Leu
435 440 445

Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu
450 455 460

Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile His Ile Ala
465 470 475 480

Ala Tyr Ala Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr Thr Phe
485 490 495

Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Ser His Leu Tyr Cys Thr Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Leu Asp Phe Lys Lys Gln Phe Asp Pro Leu Leu Pro Thr Leu
545 550 555 560

Leu Gln Gln His Leu Gly Thr Gly Leu Asp Val Asn Ala Leu Ala Leu
565 570 575

Glu Val Lys Lys Ala Leu Asn Lys Arg Leu Glu Gln Thr Thr Thr Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Tyr Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Pro Ser Ala Asn Val Thr Leu Thr
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Glu Val Arg Asn Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala
645 650 655

Pro Ala His Ala Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Gln Ala Arg Arg Gly Asp Val Phe Val
675 680 685

Gly Val Gln Gln Glu Thr Ile Gly Ser Asn Val Ser Arg Ile Tyr Glu
690 695 700

Ala Ile Lys Asp Gly Arg Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720

<210> 14
<211> 2311
<212> DNA
<213> Amanita muscaria

<220>
<221> CDS
<222> (18)...(2237)

<400> 14
gtcgctcgca aatctaa atg ggt ctc gat aac tcc aag aac act gcc aaa 50
Met Gly Leu Asp Asn Ser Lys Asn Thr Ala Lys
1 5 10

ttt ttt gac cta cca aaa gcc gtc cat ggt atg aat ggt aca acc ccc	98		
Phe Phe Asp Leu Pro Lys Ala Val His Gly Met Asn Gly Thr Thr Pro			
15	20	25	
gtc aat ggt ttt aaa gcg aca gcg ctt tcc aag gcc tcc cga aca atg	146		
Val Asn Gly Phe Lys Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met			
30	35	40	
acc aag act agc gca ctc tcg caa ttc tta gaa gcg tac cgt gaa ctc	194		
Thr Lys Thr Ser Ala Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu			
45	50	55	
gag ggc tac aag aat ggt aga gcc atc aag gtt gac ggt caa acg tta	242		
Glu Gly Tyr Lys Asn Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu			
60	65	70	75
tct att gca gcc gtc gct gca gct gct cgc tac aat gcg gcc gtt gag	290		
Ser Ile Ala Ala Val Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu			
80	85	90	
ttg gac gaa tcc cca ctt gtt aag gag cgc gtg agg aaa agt cag ctt	338		
Leu Asp Glu Ser Pro Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu			
95	100	105	
gct atc gca aac aaa gta tcg acc ggt gcc agc gta tac gga ctg tca	386		
Ala Ile Ala Asn Lys Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser			
110	115	120	
act ggt ttc ggt ggc agt gct gat aca cgg acg gac aaa ccg atg ttg	434		
Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu			
125	130	135	
ttg ggg ttt gcc ctt ttg caa cac caa cat gta ggg ata ctg ccc acc	482		
Leu Gly Phe Ala Leu Leu Gln His Gln His Val Gly Ile Leu Pro Thr			
140	145	150	155
tcg act gag cct ttg gac gtc cta cct ctc caa gat gca aat aac aca	530		
Ser Thr Glu Pro Leu Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr			
160	165	170	

agc atg cca gag gcg tgg att cgc ggg gcc att ttg atc cgt atg aat		578	
Ser Met Pro Glu Ala Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn			
175	180	185	
tcg cta att cgt ggc cac tct gga atc aga tgg gag ttg atc gaa aag		626	
Ser Leu Ile Arg Gly His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys			
190	195	200	
atg aga gaa cta ctc gcg gcc aat gtg ata cct gtc gtt ccc ctg aga		674	
Met Arg Glu Leu Leu Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg			
205	210	215	
ggc agc atc tcc tca tcc gga gat ctg tct ccc cta tcc tat atc gca		722	
Gly Ser Ile Ser Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala			
220	225	230	235
ggc acg att att ggc aac cca tca atc aag gta tat cac ggt cca tca		770	
Gly Thr Ile Ile Gly Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser			
240	245	250	
aag tcc gga att cgc caa att gga tcc tcg aag gat gtc ttg gct ctg		818	
Lys Ser Gly Ile Arg Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu			
255	260	265	
cat aat atc gaa cct ttc cca ctg gaa tcg aaa gaa cct ctt ggt att		866	
His Asn Ile Glu Pro Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile			
270	275	280	
ttg aat ggg acc gca ttc tcg gca tct gtg gca gct tta gcc cta aac		914	
Leu Asn Gly Thr Ala Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn			
285	290	295	
gaa gct atc cat ctt gtc ttg ttg gct caa gtg tgc acg gct atg ggg		962	
Glu Ala Ile His Leu Val Leu Ala Gln Val Cys Thr Ala Met Gly			
300	305	310	315
acc gag gca ttg ata ggc act cgc gct tct cat gca ccg ttc att cat		1010	
Thr Glu Ala Leu Ile Gly Thr Arg Ala Ser His Ala Pro Phe Ile His			
320	325	330	
gcc acc gca cga cca cat ccc ggt caa gta gaa tgt gct gag aac att		1058	
Ala Thr Ala Arg Pro His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile			
335	340	345	

tgg aat ttg ctc gat ggg agt aaa ttg gct cag tta gaa gag cac gaa			1106
Trp Asn Leu Leu Asp Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu			
350	355	360	
gtt cgc cta gaa gac gat aaa tac acc ctt cgg cag gac cgt tat cca			1154
Val Arg Leu Glu Asp Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro			
365	370	375	
ctc cga act tcg cct caa ttc ctt ggg cct cag att gaa gac ata atc			1202
Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile			
380	385	390	395
tcc gct ttc cag act gta acg cag gag tgt aat tac tta cca gct act			1250
Ser Ala Phe Gln Thr Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr			
400	405	410	
gac aat cca ctg att gat ggg gag act ggc gaa tct cac cac ggt ggc			1298
Asp Asn Pro Leu Ile Asp Gly Glu Thr Gly Glu Ser His His Gly Gly			
415	420	425	
aat ttc caa gcg atg gct gta act aat gca atg gag aag acg cga ctt			1346
Asn Phe Gln Ala Met Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu			
430	435	440	
gct tta cat cac gtt ggc aaa tta cta ttt tcc cag agc act gaa tta			1394
Ala Leu His His Val Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu			
445	450	455	
gtc aat cct gcg atg aac cgc ggt ctg ccg cct tca gta gct gcc aca			1442
Val Asn Pro Ala Met Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr			
460	465	470	475
gat cca tct ctc aac tac cac gcc aaa gga cta gac ata gca act gcg			1490
Asp Pro Ser Leu Asn Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala			
480	485	490	
gcc tac gta gcc gaa gcg act cct ggc ccc act cac att cag tcg gca			1538
Ala Tyr Val Ala Glu Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala			
495	500	505	

gaa atg cac aac caa gct gtt aac tcc ctg gcg ttg att tct gct cg			1586
Glu Met His Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg			
510	515	520	
gct acc atc aca tcg ttg gaa gtg cta aca tct ctg atc gcg tct tac			1634
Ala Thr Ile Thr Ser Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr			
525	530	535	
ttg tat att cta tgc caa gct ctc gac ctc cgt gcc ctt cag cgc gag			1682
Leu Tyr Ile Leu Cys Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu			
540	545	550	555
ttc ttg ccc ggt cta gac atc atc att cgt gag gag tta aga tcg tca			1730
Phe Leu Pro Gly Leu Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser			
560	565	570	
ttt gga tct ttc ctg tca tca gaa cag atg gag aaa ttg caa caa aat			1778
Phe Gly Ser Phe Leu Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn			
575	580	585	
cta act agt gca ttt gaa gat cat ctt gac aag acc acg aca atg gat			1826
Leu Thr Ser Ala Phe Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp			
590	595	600	
aat act gat cga atg act acg atg gct gct aca tca tca tca gtt cta			1874
Asn Thr Asp Arg Met Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu			
605	610	615	
ctt caa ttc ttt act gat tct ggc gcg tct gtt cct ccc tcg tct tgc			1922
Leu Gln Phe Phe Thr Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys			
620	625	630	635
gat ctt ctc tcc agt gtc tcg tcc ttc caa tct tct gtg gcg aca cgg			1970
Asp Leu Leu Ser Ser Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg			
640	645	650	
tct tca gtt ctc atg gat gac cta cgg aaa gaa tat att ttt gga gac			2018
Ser Ser Val Leu Met Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp			
655	660	665	
cgt ggc ccc acg ccc gca agc caa tac atc gga aag aca cgg cca gta			2066
Arg Gly Pro Thr Pro Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val			
670	675	680	

tac caa ttc att aga aca act ata ggc gtt cgt aag cat ggt tct gag 2114
Tyr Gln Phe Ile Arg Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu
685 690 695

aac tac aac aag ttt tat aat ggg ctg ggt gtc gaa gac gtt acc atc 2162
Asn Tyr Asn Lys Phe Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile
700 705 710 715

ggc caa aat ata tca cgc ata tac gag tca atc cgg gac ggc aaa atg 2210
Gly Gln Asn Ile Ser Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met
720 725 730

caa tcc att att gtc tcg ttg ttt gat taggtcttga aagcttgtat 2257
Gln Ser Ile Ile Val Ser Leu Phe Asp
735 740

cttattaata accatacact tcctcgaggt ctaaaaaaaaaaaaaaaa aaaaaaaa aaaa 2311

<210> 15

<211> 740

<212> PRT

<213> Amanita muscaria

<400> 15

Met Gly Leu Asp Asn Ser Lys Asn Thr Ala Lys Phe Phe Asp Leu Pro
1 5 10 15

Lys Ala Val His Gly Met Asn Gly Thr Thr Pro Val Asn Gly Phe Lys
20 25 30

Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met Thr Lys Thr Ser Ala
35 40 45

Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu Glu Gly Tyr Lys Asn
50 55 60

Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu Ser Ile Ala Ala Val
65 70 75 80

Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu Leu Asp Glu Ser Pro
85 90 95

Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu Ala Ile Ala Asn Lys
100 105 110

Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser Thr Gly Phe Gly Gly
115 120 125

Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu Leu Gly Phe Ala Leu
130 135 140

Leu Gln His Gln His Val Gly Ile Leu Pro Thr Ser Thr Glu Pro Leu
145 150 155 160

Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr Ser Met Pro Glu Ala
165 170 175

Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn Ser Leu Ile Arg Gly
180 185 190

His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys Met Arg Glu Leu Leu
195 200 205

Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg Gly Ser Ile Ser Ser
210 215 220

Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Thr Ile Ile Gly
225 230 235 240

Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser Lys Ser Gly Ile Arg
245 250 255

Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu His Asn Ile Glu Pro
260 265 270

Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile Leu Asn Gly Thr Ala
275 280 285

Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn Glu Ala Ile His Leu
290 295 300

Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly Thr Glu Ala Leu Ile
305 310 315 320

Gly Thr Arg Ala Ser His Ala Pro Phe Ile His Ala Thr Ala Arg Pro
325 330 335

His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile Trp Asn Leu Leu Asp
340 345 350

Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu Val Arg Leu Glu Asp
355 360 365

Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser Pro
370 375 380

Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile Ser Ala Phe Gln Thr
385 390 395 400

Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr Asp Asn Pro Leu Ile
405 410 415

Asp Gly Glu Thr Gly Glu Ser His His Gly Gly Asn Phe Gln Ala Met
420 425 430

Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu Ala Leu His His Val
435 440 445

Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu Val Asn Pro Ala Met
450 455 460

Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr Asp Pro Ser Leu Asn
465 470 475 480

Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala Ala Tyr Val Ala Glu
485 490 495

Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala Glu Met His Asn Gln
500 505 510

Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Ala Thr Ile Thr Ser
515 520 525

Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr Leu Tyr Ile Leu Cys
530 535 540

Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu Phe Leu Pro Gly Leu
545 550 555 560

Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser Phe Gly Ser Phe Leu
565 570 575

Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn Leu Thr Ser Ala Phe
580 585 590

Glu Asp His Leu Asp Lys Thr Thr Met Asp Asn Thr Asp Arg Met
595 600 605

Thr Thr Met Ala Ala Thr Ser Ser Val Leu Leu Gln Phe Phe Thr
610 615 620

Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys Asp Leu Leu Ser Ser
625 630 635 640

Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg Ser Ser Val Leu Met
645 650 655

Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp Arg Gly Pro Thr Pro
660 665 670

Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val Tyr Gln Phe Ile Arg
675 680 685

Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu Asn Tyr Asn Lys Phe
690 695 700

Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile Gly Gln Asn Ile Ser
705 710 715 720

Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met Gln Ser Ile Ile Val
725 730 735

Ser Leu Phe Asp
740

<210> 16
<211> 2787
<212> DNA

<213> Rhodotorula mucilaginosa

<220>

<221> CDS

<222> (646) .. (2784)

<400> 16

ctgcagaatc gccgcgacgt gacctagacc tctctttcg ccctatcgcc ctctcgac 60

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tcggcgtt cctctcctt atagacatgg gtactgatca cttcgttgt tttctcggt 180

ttctcttgca agtacgaccc atcctttttt ctcgcgtatcg acttcaatat cggtgcgc 240

gcactacgtc tcttcgcccag tgcacagttt gacgggaggg gacacgactg gcggcgaaag 300

cggagtcgtc gttgccggtc ccgagagacg ggaacacttt cttccgcctt ccagaggccg 360

tactccggtg atttgacatc gcactatgct tggggggcg cccgaactcg gagcttgcga 420

tgtgcctgaa gcagagctcg gcaggcgaca tggcgactcc gccacattcg ggtcaaagcc 480

gaagtggggc ctcggacgtt ccgaacgtcg tcttgccgcc gcccgttgc gtccggcgtc 540

gactttgtcc tcgtgtgctc acgcctcctt ctttctctt tctgcttcc tcacttcact 600

ctgcaagtcc cgcctcgcat ccacccaacc cgagcagctc tcaag atg gcc ccc tcc 657

Met Ala Pro Ser

1

gtc gac tcg atc gcg act tcg gtt gcc aac tcc ctc tcg aac ggg ttg 705

Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu Ser Asn Gly Leu

5

10

15

20

cac gcc gcc gcc gcc aac ggt ggc gac gtc cac aag aag acg gcc 753

His Ala Ala Ala Ala Asn Gly Gly Asp Val His Lys Lys Thr Ala

25

30

35

ggc gct ggc tcc ctc ctc ccg acc acc gag acg acc cag ctc gac atc 801

Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr Gln Leu Asp Ile

40

45

50

gtt gag cgc atc ttg gcc gac gcc ggc acg gac cag atc aaa ctc	849		
Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp Gln Ile Lys Leu			
55	60	65	
gat ggg tac acc ctc acg ctc ggc gac gtc gtc ggc gct gct cgc cgt	897		
Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly Ala Ala Arg Arg			
70	75	80	
ggc cgc tcc gtc aag gtc gca gac acg cac atc cgc gag aag atc	945		
Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile Arg Glu Lys Ile			
85	90	95	100
gat gcc agt gtc gag ttc ctc cgt act cag ctc gac aac agt gtc tac	993		
Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp Asn Ser Val Tyr			
105	110	115	
ggt gtc acg act ggt ttc ggc ggc tcg gcc gac acc cgg act gag gat	1041		
Gly Val Thr Thr Gly Phe Gly Ser Ala Asp Thr Arg Thr Glu Asp			
120	125	130	
gcg atc tcg ctc caa aag gcc ctg ctc gag cac cag ctc tgc ggt gtc	1089		
Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val			
135	140	145	
ctc ccc acc tcg atg gat ggc ttt ggc ctc ggt cgc ggc ctc gag aac	1137		
Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg Gly Leu Glu Asn			
150	155	160	
tcg ctt ccg ctc gaa gtc gtc cga ggc gcg atg acc atc cgt gtc aac	1185		
Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn			
165	170	175	180
tcg ctc act cgc ggt cac tcg gcg gtc cgc atc gtc gtc ctc gaa gcc	1233		
Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val Val Leu Glu Ala			
185	190	195	
ctc acc aac ttc ctc aac cac ggc atc acc ccg atc gtc ccg ctt cga	1281		
Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg			
200	205	210	

ggc acc atc tcg gcg tcg ggc gac ctt tcc ccc ctc tct tac atc gcc			1329
Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala			
215	220	225	
gcc tcg atc acc ggc cac ccg gac tcg aag gtc cac gtc gac ggc aag			1377
Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His Val Asp Gly Lys			
230	235	240	
atc atg tcc gcc cag gag gcg atc gcg ctc aag ggt ctt cag ccc gtc			1425
Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly Leu Gln Pro Val			
245	250	255	260
gtc ctc ggt ccg aag gag ggt ctc ggt ctc gtc aac ggc acg gcc gtc			1473
Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr Ala Val			
265	270	275	
tcc gcc tcg atg gcg acg ctg gcc ctc acc gac gca cac gtc ctc tcg			1521
Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala His Val Leu Ser			
280	285	290	
ctc ctc gca cag gcg ctc act gct ctt act gtc gag gcc atg gtc gga			1569
Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met Val Gly			
295	300	305	
cac gcc ggc tcg ttc cac cca ttc ctc cac gac gtc acg cgc cct cac			1617
His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg Pro His			
310	315	320	
ccg acc cag atc gag gtg gcg cgc aac atc cgg act ctt ctc gag ggc			1665
Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr Leu Leu Glu Gly			
325	330	335	340
agc aag tac gcc gtc cac cac gag act gaa gtc aag gtc aag gac gac			1713
Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys Val Lys Asp Asp			
345	350	355	
gag ggc atc ctc agg cag gac cgg tac ccg ctc cgc tgc tcg ccg cag			1761
Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Cys Ser Pro Gln			
360	365	370	
tgg ctc ggt ccc ctt gtc agc gac atg att cac gct cac gct gtc ctc			1809
Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala His Ala Val Leu			
375	380	385	

tcg ctc gag gct ggt cag tcg acc acc gac aac ccg ctg atc gac ctc	390	395	400	1857
Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile Asp Leu				
gag aac aag atg acc cac cat ggc gga gcc ttc atg gcg agc agc gtc	405	410	415	1905
Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met Ala Ser Ser Val				
gga aac acg atg gag aag act cgc ctc gcc gtc gcg ctg atg ggc aag	425	430	435	1953
Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala Leu Met Gly Lys				
gtc agc ttt act cag ctc acc gag atg ctc aac gcc ggc atg aac cgg	440	445	450	2001
Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met Asn Arg				
gcc ctt ccg tcc tgc ctc gct gcc gag gac cct tcc ctc tct tat cac	455	460	465	2049
Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser Tyr His				
tgc aag ggt ctc gac att gct gcg gcc gac tac act tcc gag ctc ggt	470	475	480	2097
Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu Leu Gly				
cac ctt gcc aac ccg gtt tcg acc cac gtc cag ccg gcc gag atg ggc	485	490	495	2145
His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro Ala Glu Met Gly				
aac cag gcc atc aac tcg ctc gcc ctc atc tcg gcc cgc cgc acc gcc	505	510	515	2193
Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala				
gag gcg aac gac gtt ctc tcc ctc ctc gcc acc cac ctc tac tgc	520	525	530	2241
Glu Ala Asn Asp Val Leu Ser Leu Leu Ala Thr His Leu Tyr Cys				
gtc ctc cag gcc gtc gac ctc cgc gcg atg gag ttt gag cac acc aag	535	540	545	2289
Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe Glu His Thr Lys				

gct ttc gag ccg atg gtc act gag ctg ttg aag cag cac ttt ggc gct	2337		
Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln His Phe Gly Ala			
550	555	560	
ctc gct acg gcc gaa gtc gag gac aag gtc cgc aag tcg atc tac aag	2385		
Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys Ser Ile Tyr Lys			
565	570	575	580
cggttg cag cag aac aac tcg tac gac ctc gag cag cgg tgg cac gac	2433		
Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln Arg Trp His Asp			
585	590	595	
acg ttc tcg gtc gct acc ggt gcc gtc gtc gag gct ctc gcc ggc cag	2481		
Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala Leu Ala Gly Gln			
600	605	610	
gag gtc tcg ctc gct acg ctc aac gcc tgg aag gtc gcc tgc gcc gag	2529		
Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val Ala Cys Ala Glu			
615	620	625	
aag gct atc gct ctc acg cgc tcc gtc cgc gac tcg ttc tgg gct	2577		
Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser Phe Trp Ala Ala			
630	635	640	
ccg tcg tcg tcg ccc gct ctc aag tac ctc tcc ccg cgg acg cgc	2625		
Pro Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser Pro Arg Thr Arg			
645	650	655	660
gtc ctg tat tcg ttc gtc cgg gag gag gtc ggc gtc aag gcc cgc cgc	2673		
Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val Lys Ala Arg Arg			
665	670	675	
ggc gat gtc tac ctc ggc aag cag gag gtc acg atc ggc acc aac gtc	2721		
Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val			
680	685	690	
acg cgc atc tac gag gct atc aag acg ggt tgc atc gcc ccc gtc ctc	2769		
Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile Ala Pro Val Leu			
695	700	705	
gtc aag atg atg gca tag	2787		
Val Lys Met Met Ala			
710			

<210> 17

<211> 713

<212> PRT

<213> Rhodotorula mucilaginosa

<400> 17

Met Ala Pro Ser Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu
1 5 10 15

Ser Asn Gly Leu His Ala Ala Ala Ala Asn Gly Gly Asp Val His
20 25 30

Lys Lys Thr Ala Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr
35 40 45

Gln Leu Asp Ile Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp
50 55 60

Gln Ile Lys Leu Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly
65 70 75 80

Ala Ala Arg Arg Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile
85 90 95

Arg Glu Lys Ile Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp
100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Val Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
210 215 220

Ser Tyr Ile Ala Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His
225 230 235 240

Val Asp Gly Lys Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly
245 250 255

Leu Gln Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn
260 265 270

Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala
275 280 285

His Val Leu Ser Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu
290 295 300

Ala Met Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val
305 310 315 320

Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr
325 330 335

Leu Leu Glu Gly Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys
340 345 350

Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg
355 360 365

Cys Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala
370 375 380

His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro
385 390 395 400

Leu Ile Asp Leu Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met
405 410 415

Ala Ser Ser Val Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala
420 425 430

Leu Met Gly Lys Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala
435 440 445

Gly Met Asn Arg Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser
450 455 460

Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr
465 470 475 480

Ser Glu Leu Gly His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro
485 490 495

Ala Glu Met Gly Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala
500 505 510

Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Ala Thr
515 520 525

His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe
530 535 540

Glu His Thr Lys Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln
545 550 555 560

His Phe Gly Ala Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys
565 570 575

Ser Ile Tyr Lys Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln
580 585 590

Arg Trp His Asp Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala
595 600 605

Leu Ala Gly Gln Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val
610 615 620

Ala Cys Ala Glu Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser
625 630 635 640

Phe Trp Ala Ala Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser
645 650 655

Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val
660 665 670

Lys Ala Arg Arg Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile
675 680 685

Gly Thr Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile
690 695 700

Ala Pro Val Leu Val Lys Met Met Ala
705 710

<210> 18

<211> 2439

<212> DNA

<213> Rhodotorula toruloides

<220>

<221> CDS

<222> (1)..(2148)

<400> 18

atg gca ccc tcg ctc gac tcg atc tcg cac tcg ttc gca aac ggc gtc 48
Met Ala Pro Ser Leu Asp Ser Ile Ser His Ser Phe Ala Asn Gly Val
1 5 10 15

gca tcc gca aag cag gct gtc aat ggc gcc tcg acc aac ctc gca gtc 96
Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

gca ggc tcg cac ctg ccc aca acc cag gtc acg cag gtc gac atc gtc 144
Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
35 40 45

gag aag atg ctc gcc gcg acc gac tcg acg ctc gaa ctc gac ggc 192
Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
50 55 60

tac tcg ctc aac ctc gga gac gtc gtc tcg gcc gcg agg aag ggc agg	240		
Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg			
65	70	75	80
cct gtc cgc gtc aag gac agc gac gag atc cgc tca aag att gac aaa	288		
Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys			
85	90	95	
tcg gtc gag ttc ttg cgc tcg caa ctc tcc atg agc gtc tac ggc gtc	336		
Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val			
100	105	110	
acg act gga ttt ggc gga tcc gca gac acc cgc acc gag gac gcc atc	384		
Thr Thr Gly Phe Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile			
115	120	125	
tcg ctc cag aag gct ctc ctc gag cac cag ctc tgc ggt gtt ctc cct	432		
Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro			
130	135	140	
tcg tcg ttc gac tcg ttc cgc ctc ggc cgc ggt ctc gag aac tcg ctt	480		
Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu			
145	150	155	160
ccc ctc gag gtt gtt cgc ggc gcc atg aca atc cgc gtc aac agc ttg	528		
Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu			
165	170	175	
acc cgc ggc cac tcg gct gtc cgc ctc gtc ctc gag gcg ctc acc	576		
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr			
180	185	190	
aac ttc ctc aac cac ggc atc acc ccc atc gtc ccc ctc cgc ggc acc	624		
Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr			
195	200	205	
atc tct gcg tcg ggc gac ctc tct cct ctc tcc tac att gca gcg gcc	672		
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala			
210	215	220	

atc	agc	ggt	cac	ccg	gac	agc	aag	gtg	cac	gtc	cac	gag	ggc	aag	720		
Ile	Ser	Gly	His	Pro	Asp	Ser	Lys	Val	His	Val	Val	His	Glu	Gly	Lys		
225															240		
230															235		
245															250		
255															268		
gag	aag	atc	ctg	tac	gcc	cg	gag	g	atg	g	cg	ctc	ttc	aac	ctc	gag	720
Glu	Lys	Ile	Leu	Tyr	Ala	Arg	Glu	Ala	Met	Ala	Leu	Phe	Asn	Leu	Glu		
245																255	
ccc	gtc	gtc	ctc	ggc	ccg	aag	gaa	ggt	ctc	gg	ctc	gtc	aac	ggc	acc	816	
Pro	Val	Val	Leu	Gly	Pro	Lys	Glu	Gly	Leu	Gly	Leu	Val	Asn	Gly	Thr		
260																270	
275																285	
gcc	gtc	tca	gca	tcg	atg	gcc	acc	ctc	gct	ctg	cac	gac	gca	cac	atg	864	
Ala	Val	Ser	Ala	Ser	Met	Ala	Thr	Leu	Ala	Leu	His	Asp	Ala	His	Met		
275																285	
ctc	tcg	ctc	tcg	cag	tcg	ctc	acg	gcc	atg	acg	gtc	gaa	g	cg	atg	912	
Leu	Ser	Leu	Ser	Gln	Ser	Leu	Thr	Ala	Met	Thr	Val	Glu	Ala	Met			
290																300	
300																300	
gtc	ggc	cac	gcc	ggc	tcg	ttc	cac	ccc	ttc	ctt	cac	gac	gtc	acg	cg	960	
Val	Gly	His	Ala	Gly	Ser	Phe	His	Pro	Phe	Leu	His	Asp	Val	Thr	Arg		
305																320	
cct	cac	ccg	acg	cag	atc	gaa	gtc	g	cg	g	a	ac	atc	cc	ctc	1008	
Pro	His	Pro	Thr	Gln	Ile	Glu	Val	Ala	Gly	Asn	Ile	Arg	Lys	Leu	Leu		
325																330	
325																330	
gag	gga	agc	cg	ttt	gt	c	ac	cat	gag	gag	gag	gtc	aag	gtc	aag	1056	
Glu	Gly	Ser	Arg	Phe	Ala	Val	His	His	Glu	Glu	Glu	Val	Lys	Val	Lys		
340																350	
340																350	
gac	gac	gag	ggc	att	ctc	cg	cag	gac	cg	tc	cc	tt	cg	ac	tct	1104	
Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	Arg	Tyr	Pro	Leu	Arg	Thr	Ser		
355																365	
355																365	
cct	cag	tgg	ctc	ggc	ccg	ctc	gtc	agc	gac	ctc	att	cac	gcc	cac	ggc	1152	
Pro	Gln	Trp	Leu	Gly	Pro	Leu	Val	Ser	Asp	Leu	Ile	His	Ala	His	Ala		
370																380	
375																380	
gtc	ctc	acc	atc	gag	gcc	ggc	cag	tcg	acg	acc	gac	aac	cct	ctc	atc	1200	
Val	Leu	Thr	Ile	Glu	Ala	Gly	Gln	Ser	Thr	Thr	Asp	Asn	Pro	Leu	Ile		
385																400	
390																400	

gac gtc gag aac aag act tcg cac cac ggc ggc aat ttc cag gct gcc		1248	
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala			
405	410	415	
gct gtg gcc aac acc atg gag aag act cgc ctc ggg ctc gcc cag atc		1296	
Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile			
420	425	430	
ggc aag ctc aac ttc acg cag ctc acc gag atg ctc aac gcc ggc atg		1344	
Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met			
435	440	445	
aac cgc ggc ctc ccc tcc tgc ctc gcg gcc gaa gac ccc tcg ctc tcc		1392	
Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser			
450	455	460	
tac cac tgc aag ggc ctc gac atc gcc gct gcg tac acc tcg gag		1440	
Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu			
465	470	475	480
ttg gga cac ctc gcc aac cct gtg acg acg cat gtc cag ccg gct gag		1488	
Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu			
485	490	495	
atg gcg aac cag gcg gtc aac tcg ctt gcg ctc atc tcg gct cgt cgc		1536	
Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg			
500	505	510	
acg acc gag tcc aac gac gtc ctt tct ctc ctc gcc acc cac ctc		1584	
Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Ala Thr His Leu			
515	520	525	
tac tgc gtt ctc caa gcc atc gac ttg cgc gcg atc gag ttc gag ttc		1632	
Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe			
530	535	540	
aag aag cag ttc ggc cca gcc atc gtc tcg ctc atc gac cag cac ttt		1680	
Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe			
545	550	555	560

ggc tcc gcc atg acc ggc tcg aac ctg cgc gac gag ctc gtc gag aag			1728
Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys			
565	570	575	
gtg aac aag acg ctc gcc aag cgc ctc gag cag acc aac tcg tac gac			1776
Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp			
580	585	590	
ctc gtc ccg cgc tgg cac gac gcc ttc tcc ttc gcc gcc ggc acc gtc			1824
Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val			
595	600	605	
gtc gag gtc ctc tcg acg tcg ctc tcg ctc gcc gcc gtc aac gcc			1872
Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala			
610	615	620	
tgg aag gtc gcc gcc gag tcg gcc atc tcg ctc acc cgc caa gtc			1920
Trp Lys Val Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val			
625	630	635	640
cgc gag acc ttc tgg tcc gcc gcg tcg acc tcg tcg ccc gcg ctc tcg			1968
Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser			
645	650	655	
tac ctc tcg ccg cgc act cag atc ctc tac gcc ttc gtc cgc gag gag			2016
Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu			
660	665	670	
ctt ggc gtc aag gcc cgc cgc gga gac gtc ttc ctc ggc aag caa gag			2064
Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu			
675	680	685	
gtg acg atc ggc tcg aac gtc tcc aag atc tac gag gcc atc aag tcg			2112
Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser			
690	695	700	
ggc agg atc aac aac gtc ctc ctc aag atg ctc gct tagacactct			2158
Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala			
705	710	715	
tcccaactctc gcatcccttc cataccctat cccgcctgca ctcttaggac tcgcttcttg			2218
tcggactcgg atctcgcatc gcttcttcg ttcttgctg cctctctaga ccgtgtccgt			2278

attacctcg a gattgtgaat acaagcagta cccatccacg catccgataa atcagggaga 2338
gaatctacgc ttgcgggagc ttcttgcgca taaactgtcg agtgcgggag tttagtgcgaa 2398
gtcaacgaag gcgagtgccgca gcggctcact accgcctcg a g 2439

<210> 19
<211> 716
<212> PRT
<213> Rhodotorula toruloides

<400> 19

Met Ala Pro Ser Leu Asp Ser Ile Scr His Ser Phe Ala Asn Gly Val
1 5 10 15

Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
35 40 45

Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
50 55 60

Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg
65 70 75 80

Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys
85 90 95

Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val
100 105 110

Thr Thr Gly Phe Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile
115 120 125

Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro
130 135 140

Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu
145 150 155 160

Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu
165 170 175

Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr
180 185 190

Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr
195 200 205

Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala
210 215 220

Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys
225 230 235 240

Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu
245 250 255

Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr
260 265 270

Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met
275 280 285

Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met
290 295 300

Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg
305 310 315 320

Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu
325 330 335

Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys
340 345 350

Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser
355 360 365

Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala
370 375 380

Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile
385 390 395 400

Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala
405 410 415

Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile
420 425 430

Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met
435 440 445

Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser
450 455 460

Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu
465 470 475 480

Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu
485 490 495

Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg
500 505 510

Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Ala Thr His Leu
515 520 525

Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe
530 535 540

Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe
545 550 555 560

Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys
565 570 575

Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp
580 585 590

Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val
595 600 605

Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
610 615 620

Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625 630 635 640

Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
645 650 655

Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
660 665 670

Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
675 680 685

Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
690 695 700

Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala
705 710 715

<210> 20

<211> 2475

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_difference

<222> (13) .. (2475)

<223> n = A or C or G or T; "n" indicates no consensus at that position

<223> Description of Artificial Sequence: Consensus
Sequence of SEQ ID NOS: 12, 16, and 18

<400> 20

atggcccccct ccntcgactc gatcgcgacc tcgntcgcca acggcncnc naacggntng 60

cacggcgnnc cgncnnngnc gncnacgggc gccacgtcca cnctcngncg gccgnncgng 120
gctcgctcct cccgaccacc cagnngacgc agctcgacat cgtngagnag atcctcgccg 180
accccacccgn nacgnacgnn ntcgaactcg acgggtacac cctcaccctc ggngacgtcg 240
tcggcgccgc ncgcaagggc cgcnengtcc gcgtcncaga cagnngacga gatcccgca 300
aagatcgaca anagngtcga gttcctccgn ncncagctn acaacagngt ctacggngtc 360
acgactggtt tcggcggtc ggccgacacc cggactgagg atgcnatctc gctccagaag 420
gcncctcctcg agcaccagct ctgcgggtgn ctcccnaacgt cgntcgantc cttcngcctc 480
ggncgcggcc tcgagaactc gttccgctc gaggtcggtcc gcccgcacat gaccatccgc 540
gtcaactcgc tcacncgcgg ccactcggcn gtccgcctcg tgcgtcctcg ggcgctcacc 600
aacttcctca accacggcat caccatccatc gtcccccctcc gcccgcacat ctccggcgtcg 660
ggcgacctct ccccnctctc ntacatcgcc gcccgcacatc ccggtcaccc ggacnncaag 720
gtncacgttn tncacgaggg canngagaag atcatgtncg cccgcgaggg gatcgcgctc 780
ttnggtctcg agcccggtcg cctcgcccg aaggagggtc tgggtctcgta caacggcacc 840
gccgtctccg cctcgatggc gaccctcgct ctgcacgacg cacacatgtc ctccgtcctc 900
tcgcaggcgc tcacggctct nacggtcag gccatggtcg gcccgcggg ctccgttccac 960
ccnttcctcc acgacgtcac gcccgcacatc ccgaccatc tcgaggtcg gcccgcacatc 1020
cgcacgctcc tcgagggcag cnngttgcc gtccaccacg aggaggaggt caaggtcaag 1080
gacgacgagg gcattctccg ccaggaccgc taccgcgtcc gcacgtcgcc tcagtggtc 1140
ggcccgctcg tcagcgacat gattcagcc cacgcngtcc tctcgctcgaa ggccggncag 1200
tcgacgaccgc acaacccgt catcgacgtc gagaacaaga ngaccacca cggcggcaac 1260
ttccaggcgn ccgctgtcg naacacgtg gagaagactc gcctcgcnct cggccgtac 1320
ggcaagctca acttcacgca gtcaccgag atgctcaacg ccggcatgaa cccggccctn 1380

ccntcctgcc tcgctgccga ggaccctntcg ctctcctatc actgcaaggg cctcgacatt 1440
gcccgcngcng cntacacttc ggagctcggn caccttgcca acccggtac gacccacgtc 1500
cagccggcng agatggcaa ccaggccgtc aactcgctcg cnctcatctc ggcnccgcgc 1560
acngccgagg ccaacgacgt cctttctctc ctccctcgcca cccacctcta ctgcgtntc 1620
cagggccgtcg acctccgcgc gatggagttc gagttcaaga agcagttcga cccgntnnntc 1680
ncnnncgctcn tcnagcagca ctggcnncn gccctcgacg gcnnnnnnnn nnnnnacgaa 1740
ctcgnggaca aggtcaacaa gncgctcnac aagcgncgtc agcagaccaa ctcgtacgac 1800
ctcgagccgc gctggcacga cgccttctcg ttgcgcaccc gcaccgtcgt cgagnnnnnn 1860
nnngtctcgc cnnnngccan naggtctcgc tcgcngccgt caacgcctgg aaggtcgct 1920
ccgcccggagaa ggccatctcg ctcacgcgcn angtccgcga cnccttctgg nccggcncgt 1980
cgtcgctcgcc gccccgcgtc ncgtacctct cgcgcgcac gcgcgtcctg tactcggtcg 2040
tccgcgagga gctcgccgtc aaggcccgcc gcggcgacgt ctgcctcgcc aagcaggagg 2100
tgacgatcg caccacgtc tcccgcatct acgaggccat caagnncgac ngtcgatcaacc 2160
acgtcctcgta caagatgctc gcntagnnnnc ncnnncnann ctgcntnnn ncnnnnncnc 2220
nnnccnnnnn nnntnttng nnntcgntc ntgnccnnnnn cgganntnnnc nnncnnnnnnn 2280
tnnnncntnn ctnnctcnncn nnnancnngt cnntnnnnnc tnnngnntnn nnncnnncnnnc 2340
ngtnnnncann nacncntnnn nnnannncngg nanngantnn angnntncgn gnnccnnnnnn 2400
nnnnanaaann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2460
nnnnnnnnnnn nnnnn 2475
<210> 21
<211> 726
<212> PRT
<213> Artificial Sequence

<220>

<221> SITE

<222> (12)...(719)

<223> "Xaa" means any amino acid; "Xaa" means no consensus at that position

<223> Description of Artificial Sequence: Consensus of
SEQ ID NOS: 13, 17, and 19

<400> 21

Met Ala Pro Ser Leu Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

Xaa Asn Gly Xaa His Ala Ala Xaa Xaa Ala Ser Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Ala Xaa Ala Gly Ser Xaa Leu Pro Thr Thr Xaa Xaa
35 40 45

Thr Gln Leu Asp Ile Val Glu Xaa Xaa Leu Ala Asp Pro Xaa Thr Asp
50 55 60

Asp Xaa Xaa Glu Leu Asp Gly Tyr Ser Leu Thr Leu Gly Asp Val Val
65 70 75 80

Gly Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Xaa Asp Ser Asp Glu
85 90 95

Ile Arg Xaa Lys Ile Asp Lys Ser Val Glu Phe Leu Arg Xaa Gln Leu
100 105 110

Xaa Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Ser Ala Asp
115 120 125

Thr Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His
130 135 140

Gln Leu Cys Gly Val Leu Pro Thr Ser Xaa Asp Ser Phe Xaa Leu Gly
145 150 155 160

Arg Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met
165 170 175

Thr Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu
180 185 190

Val Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro
195 200 205

Ile Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro
210 215 220

Leu Ser Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Ser Lys Val
225 230 235 240

His Val Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala
245 250 255

Ile Ala Leu Phe Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly
260 265 270

Leu Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu
275 280 285

Ala Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr
290 295 300

Ala Leu Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Pro
305 310 315 320

Phe Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala
325 330 335

Arg Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His
340 345 350

Glu Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp
355 360 365

Arg Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser
370 375 380

Asp Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser
385 390 395 400

Thr Thr Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His
405 410 415

Gly Gly Asn Phe Gln Ala Ser Ala Val Xaa Asn Thr Met Glu Lys Thr
420 425 430

Arg Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr
435 440 445

Glu Met Leu Asn Ala Gly Met Asn Arg Gly Leu Pro Ser Cys Leu Ala
450 455 460

Ala Glu Asp Pro Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala
465 470 475 480

Ala Ala Ala Tyr Thr Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr
485 490 495

Thr His Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu
500 505 510

Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser
515 520 525

Leu Leu Leu Ala Thr His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu
530 535 540

Arg Ala Met Glu Phe Glu Phe Lys Lys Gln Phe Xaa Pro Xaa Xaa Xaa
545 550 555 560

Xaa Leu Leu Xaa Gln His Phe Gly Xaa Xaa Xaa Thr Xaa Xaa Xaa
565 570 575

Xaa Xaa Glu Leu Xaa Xaa Lys Val Xaa Lys Xaa Leu Xaa Lys Arg Leu
580 585 590

Glu Gln Thr Asn Ser Tyr Asp Leu Glu Pro Arg Trp His Asp Ala Phe
595 600 605

Ser Xaa Ala Thr Gly Thr Val Val Glu Xaa Leu Ser Ser Xaa Xaa Xaa
610 615 620

Xaa Xaa Val Ser Leu Ala Ala Val Asn Ala Trp Lys Val Ala Xaa Ala
625 630 635 640

Glu Lys Ala Ile Ser Leu Thr Arg Xaa Val Arg Xaa Xaa Phe Trp Xaa
645 650 655

Ala Pro Ser Ser Ser Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr
660 665 670

Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val Lys Ala Arg
675 680 685

Arg Gly Asp Val Phe Leu Gly Lys Gln Glu Val Thr Ile Gly Ser Asn
690 695 700

Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Arg Ile Asn Xaa Val
705 710 715 720

Leu Val Lys Met Leu Ala
725

<210> 22

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 74

<400> 22

atccatatgg ctccttcttt ggattctctt gctactacgc tcgcacacgg ctttacc 57

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 75

<400> 23

atcgccggccg catgcggatc ctcattacgc gagcatctt acgaggacgt ggttgatgcg 60
<210> 24
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 105

<400> 24
agtgaattca tggccccc ttc cttggactcg ctcgcca

37

<210> 25
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 80

<400> 25
atcgcatgt cattacgcga gcatcttgac gaggacgtgg ttgatgcg
<210> 26
<211> 39
<212> DNA
<213> Artificial

48

<220>
<223> Description of Artificial Sequence: oli 89

<400> 26
taaaagatct ccaccatggc cccttccttg gactcgctc
39

<210> 27
<211> 36

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: oli 90

<400> 27

caagcggccg cagagacgct ggatacgaaa gaaactg
36

<210> 28

<211> 2741

<212> DNA

<213> Rhodotorula graminis

<220>

<221> modified_base

<222> (6)

<223> Description of modified_base: m = a or c

<220>

<221> exon

<222> (2008) .. (2586)

<223>

<220>

<221> exon

<222> (1822) .. (1947)

<223>

<220>

<221> exon

<222> (1587) .. (1748)

<223>

<220>

<221> exon

<222> (1365)..(1529)

<223>

<220>

<221> exon

<222> (961)..(1295)

<223>

<220>

<221> exon

<222> (449)..(880)

<223>

<220>

<221> exon

<222> (1)..(361)

<223>

<220>

<221> terminator

<222> (2587)..(2589)

<223>

<220>

<221> Intron

<222> (1948)..(2007)

<223>

<220>

<221> Intron

<222> (1749) .. (1821)

<223>

<220>

<221> Intron

<222> (1530) .. (1586)

<223>

<220>

<221> Intron

<222> (1296) .. (1364)

<223>

<220>

<221> Intron

<222> (881) .. (960)

<223>

<220>

<221> Intron

<222> (362) .. (448)

<223>

<400> 28

atg gcm cct tcc ttg gac tcg ctc gcc acc acg ctc gcc aac ggc ttt 48

Met Ala Pro Ser Leu Asp Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe

1

5

10

15

acc aac ggc tcg cac gcc gct ccg acc aag tcg gct gcg ggc ccc act 96

Thr Asn Gly Ser His Ala Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr

20

25

30

tcg gct ctc cgc cgc acg ccc ggc ctc gat ggc cac gcc gcg cac cag	35	40	45	144
Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln				
tcg cag ctc gag atc gtg cag gag ctc ctc agc gac ccc acc gac gac	50	55	60	192
Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp				
gtc gtc gag ctc agc ggg tac agc ctc acc gtc cgt gac gtt gtc ggc	65	70	75	240
Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly				
gcc gcc cgc aag ggg cgc agg gtc cgc gtc cag aac gac gac gag atc	85	90	95	288
Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile				
cgc gca cgc gtc gac aag agc gtc gac ttc ctc aag gcc cag ctt cag	100	105	110	336
Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln				
aac tcg gtc tac gga gtc acc acg g tgcggtccga gacgagagggc	115	120		381
Asn Ser Val Tyr Gly Val Thr Thr				
ggaaatctcg ggatgccgca ggcgtgaacg ctgacactcg cttggacggc tgccgcggc				441
ttgcagg gt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc	125	130		489
Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val				
agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg	135	140	145	537
Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro				

acg tcc gtc tcg tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt	585		
Thr Ser Val Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu			
155	160	165	
ccg ctc gag gtc gtc cgc ggc gcc atg gtc atc cgc gtc aac tcg ctc	633		
Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu			
170	175	180	
acg cgt ggc cac tcg gcc gtc cgc ctc gtc ctt gag gcg ctc acc	681		
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr			
185	190	195	
aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc ggc tcc	729		
Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser			
200	205	210	
atc tcg gcg tcg ggc gac ctc agc ccg ctc tcg tac atc gcc ggc gcc	777		
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala			
215	220	225	230
atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc	825		
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr			
235	240	245	
gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag	873		
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu			
250	255	260	
gca gtc g gtacgtcgcg agtcctgact gcagtgagct gttcgagagt ctcccagtt	930		
Ala Val			

gctgactgcc ctttgttcat gcgattgcag tc ctc ggc ccg aag gag ggt ctc 983
Val Leu Gly Pro Lys Glu Gly Leu
270

ggt ctg gtc aac gga acg gcc gtc tcc gcc tcg atg gcg acc ctc agt 1031
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
275 280 285

ctg cac gac tcg cac atg ctc tcg ctc tcg cag gcc ttg acg gct 1079
Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

ctc acg gtg gag gcc atg gtc ggc cag cag ggc tcg ttc gcg ccg ttc 1127
Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
305 310 315 320

atc cac gac gtc tgc cgc ccg cac ccc ggc cag gtc gag gtc gcg cgc 1175
Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
325 330 335

aac atc cgc acg ctc ctt tcc ggc tcg tcg ttt gcc gtt gag cac gag 1223
Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
340 345 350

gag gag gtc aag gtc aag gac gac gag ggc att ctt cgc cag gac cgc 1271
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

tac ccg ctc cgc acg tcg cct cag gttcgcccc tctctctccc cttccctccg 1325
Tyr Pro Leu Arg Thr Ser Pro Gln
370 375

tccgaccggc gcgtcgagac ttacgaaaa cgtatccag ttc ctc ggc ccg ctc 1379
Phe Leu Gly Pro Leu
380

gtg gag gac atg atg cac gcc tac tcg act ctc tcg ctc gag aac aac 1427
Val Glu Asp Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn
385 390 395

acg acg acc gac aac ccg ctc ctc gac gtc gag aac aag cag acc gcg 1475
Thr Thr Thr Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala
400 405 410

cac ggc ggc aac ttc cag gcg tcg gct gtc tcg att tcg atg gag aag 1523
His Gly Gly Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys
415 420 425

acc agg tgcgtctctc gctgccttcg tactccgatc ttgtgctgaa tggctttctc 1579
Thr Arg
430

ctgcagg ctc gca ctc gcc ctc atc ggc aag ctc aac ttc acg cag tgc 1628
Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys
435 440 445

acc gag ttg ctc aac gct gcc atg aac cgc ggc ctg cct tcg tgc ctc 1676
Thr Glu Leu Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu
450 455 460

gct gcc gag gac ccg tcg ctc aac tat cac ggc aag ggc ttg gac att 1724
Ala Ala Glu Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile
465 470 475

cac atc gct gct tac tcg gag gtgagccgtc gacgttctcc gccgtcgctc 1778
His Ile Ala Ala Tyr Ala Ser Glu

480 485

gtccccttca ggcgcacccag gctgacttcc tttccctctg tag ctc ggc cac ctt 1833
Leu Gly His Leu

gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg ggc aac cag 1881
Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met Gly Asn Gln
490 495 500 505

gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act gcc gag gcc 1929
Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala
510 515 520

aac gac gtc ctt tct ctc gtgcgttcgt gtcgcaatga gtcccgacgc 1977
Asn Asp Val Leu Ser Leu
525

aatagcgact gactgcgcga tcctgagcag ctt ctc gcc tcg cac ctg tac tgc 2031
Leu Leu Ala Ser His Leu Tyr Cys
530 535

acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag aag 2079
Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys Lys
540 545 550

cag ttc gac ccg ctt ctc ccg act ctc ctc cag cag cac ctc ggc act 2127
Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly Thr
555 560 565

ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc aac 2175
Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu Asn
570 575 580

aag cgt ctc gag cag acg acg tac gac ctc gag ccg cgc tgg cac 2223
Lys Arg Leu Glu Gln Thr Thr Tyr Asp Leu Glu Pro Arg Trp His
585 590 595

gac gcc ttc tcg tac gcg acc ggc acc gtc gtc gag ctc ctc tcg tcc 2271
Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser Ser
600 605 610 615

tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag gtt 2319
Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys Val
620 625 630

gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac cgc 2367
Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn Arg
635 640 645

tcc tgg cag acg ccg tct tcg cag gcg ccg gcg cac gca tac ctc tcg 2415
Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu Ser
650 655 660

ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc ggc gtg 2463
Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val
665 670 675

cag gcg cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg atc 2511
Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr Ile
680 685 690 695

ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc atc 2559
Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg Ile
700 705 710

aac cac gtc ctc gtc aag atg ctc gcg taaggcccg a gcaaggctcg 2606
Asn His Val Leu Val Lys Met Leu Ala
715 720

ccttagacgcc cgccctcaccc caagaccaggc ttttcgacgt cgtgtcgtgc caagaacgga 2666

ctttcctcca tacacatgtc gtcttactct ctcgcccgtca tcacgtctct cagtttttc 2726

gtatcccgcg tctct 2741

<210> 29
<211> 2163
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Preferred

theoretical sequence based in part on SEQ ID NO:20

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<222> (1)..(2163)
<223>

<400> 29
atg gcc ccc tcc btc gac tcg atc gcg acc tcg btc gcc aac ggc btc 48
Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

dcv aac ggv thg cac gcc gct ccg hcc aag ycg scw acg ggc gcc acg 96
Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
20 25 30

tcc ach ctc mgm cgg ccg bcc dgg ctc gct cct ccc gcc acc cag vhg 144
Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
35 40 45

acg cag ctc gac atc gtb gag vag atc ctc gcc gac ccc acc gac gac	192
Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp	
50 55 60	
gws vtc gaa ctc gac ggg tac acc ctc acc ctc ggh gac gtc gtc ggc	240
Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly	
65 70 75 80	
gcc gcb cgc aag ggc cgc hcb gtc cgc gtc cag aca gmc gac gag atc	288
Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile	
85 90 95	
cgc gca aag atc gac aav agb gtc gag ttc ctc cgb dcg cag ctc bac	336
Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa	
100 105 110	
aac agb gtc tac ggh gtc acg act ggt ttc ggc ggc tcg gcc gac acc	384
Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr	
115 120 125	
cgg act gag gat gcv atc tcg ctc cag aag gcb ctc ctc gag cac cag	432
Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln	
130 135 140	
ctc tgc ggt gtb ctc ccb acg tcg dtc gab tcc ttc vgc ctc ggh cgc	480
Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg	
145 150 155 160	
ggc ctc gag aac tcg ctt ccg ctc gag gtc gtc cgc ggc gcc atg acc	528
Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr	
165 170 175	
atc cgc gtc aac tcg ctc acb cgc ggc cac tcg gcb gtc cgc ctc gtc	576
Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val	
180 185 190	
gtc ctc gag gcg ctc acc aac ttc ctc aac cac ggc atc acc ccc atc	624
Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile	
195 200 205	
gtc ccc ctc cgc ggc acc atc tcg gcg tcg ggc gac ctc tcc ccb ctc	672
Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu	
210 215 220	
tcb tac atc gcc gcc acc atc acc ggt cac ccg gac dbc aag gtb cac	720
Xaa Tyr Ile Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His	
225 230 235 240	
gty kts cac gag ggc ams gag aag atc atg thc gcc cgc gag ggc atc	768
Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile	
245 250 255	

gag ctc ttg ggt ctc gag ccc gtc gtc ctc ggc ccg aag gag ggt ctc		816	
Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu			
260	265	270	
ggt ctc gtc aac ggc acg gcc gtc tcc gcc tcg atg gag acc ctc gct		864	
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala			
275	280	285	
ctg cac gac gca cac atg ctc tcg ctc tcg cag ggc ctc acg gct		912	
Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala			
290	295	300	
ctb acg gtc gag gcc atg gtc ggc cac gcc ggc tcg ttc cac ccv ttc		960	
Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe			
305	310	315	320
ctc cac gac gtc acg cgc cct cac ccg acc cag atc gag gtc ggc cgc		1008	
Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg			
325	330	335	
aac atc cgc acg ctc ctc gag ggc agc hvg ttt gcc gtc cac cac gag		1056	
Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu			
340	345	350	
gag gag gtc aag gtc aag gac gac gag ggc att ctc cgc cag gac cgc		1104	
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg			
355	360	365	
tac ccg ctc cgc acg tcg cct cag tgg ctc ggc ccg ctc gtc agc gac		1152	
Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp			
370	375	380	
atg att cac gcc cac gcb gtc ctc tcg ctc gag gcc gag tcg acg acc		1200	
Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr			
385	390	395	400
gac aac ccg ctc atc gac gtc gag aac aag ahg acc cac cac ggc ggc		1248	
Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly			
405	410	415	
aac ttc cag gcg dcc gct gtc gcv aac acg atg gag aag act cgc ctc		1296	
Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu			
420	425	430	
gcv ctc gcc ctg atc ggc aag ctc aac ttc acg cag ctc acc gag atg		1344	
Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met			
435	440	445	
ctc aac gcc ggc atg aac cgc ggc ctb ccb tcc tgc ctc gct gcc gag		1392	
Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu			
450	455	460	

gac ccb tcg ctc tcc tat cac tgc aag ggc ctc gac att gcc gcb gcb Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala 465	470	475	480	1440
gcb tac act tcg gag ctc ggh cac ctt gcc aac ccg gtb acg acc cac Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His 485	490	495		1488
gtc cag ccg gch gag atg ggc aac cag gcc gtc aac tcg ctc gcb ctc Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu 500	505	510		1536
atc tcg gcb cgc cgc acb gcc gag gcc aac gac gtc ctt tct ctc ctc Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu 515	520	525		1584
ctc gcc acc cac ctc tac tgc gtb ctc cag gcc gtc gac ctc cgc gcg Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala 530	535	540		1632
atg gag ttc gag ttc aag aag cag ttc gac ccg vtb vtc vcb dcg ctc Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu 545	550	555	560	1680
htc vag cag cac ttt ggc dcy gcc ctc gac ggc wac gaa ctc ghh gac Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp 565	570	575		1728
aag gtc aac aag dcg ctc dac aag cgb ctc gag cag acc aac tcg tac Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr 580	585	590		1776
gac ctc gag ccg cgc tgg cac gac gcc ttc tcg ttc gcg acc ggc acc Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr 595	600	605		1824
gtc gtc gag ctc ctc tcg tcc tcg ccb yct gcc aag gtc tcg ctc gcb Val Val Glu Leu Leu Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala 610	615	620		1872
gcc gtc aac gcc tgg aag gtc gcc tcc gcc gag aag gcc atc tcg ctc Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu 625	630	635	640	1920
acg cgc bac gtc cgc gac hcc ttc tgg bcg gcb ccg tcg tcg tcg tcg Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser 645	650	655		1968
ccc gcg ctc dcg tac ctc tcg ccg cgc acg ccg gtc ctg tac tcg ttc Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe 660	665	670		2016

gtc cgc gag gag ctc ggc gtc aag gcc cgc cgc gac gtc ttc ctc 2064
Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
675 680 685

ggc aag cag gag gtg acg atc ggc acc aac gtc tcc cgc atc tac gag 2112
Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
690 695 700

gcc atc aag dvc ggc hgc atc aac cac gtc ctc gtc aag atg ctc gcd 2160
Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720

tag 2163

<210> 30
<211> 720
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Preferred
theoretical sequence based in part on SEQ ID NO:20

<220>
<221> misc_feature
<222> (5)..(5)
<223> The 'Xaa' at location 5 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (12)..(12)
<223> The 'Xaa' at location 12 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (16)..(16)
<223> The 'Xaa' at location 16 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (17)..(17)
<223> The 'Xaa' at location 17 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (19)..(19)
<223> The 'Xaa' at location 19 stands for Gly.

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<220>
<221> misc_feature
<222> (20)..(20)
<223> The 'Xaa' at location 20 stands for a stop codon, Ser, or Leu.

<220>
<221> misc_feature
<222> (25)..(25)
<223> The 'Xaa' at location 25 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (27)..(27)
<223> The 'Xaa' at location 27 stands for Pro, or Ser.

<220>
<221> misc_feature
<222> (28)..(28)
<223> The 'Xaa' at location 28 stands for Ala, or Pro.

<220>
<221> misc_feature
<222> (34)..(34)
<223> The 'Xaa' at location 34 stands for Thr.

<220>
<221> misc_feature
<222> (36)..(36)
<223> The 'Xaa' at location 36 stands for Arg, or Ser.

<220>
<221> misc_feature
<222> (39)..(39)
<223> The 'Xaa' at location 39 stands for Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> (40)..(40)
<223> The 'Xaa' at location 40 stands for Arg, Gly, or Trp.

<220>
<221> misc_feature
<222> (48)..(48)
<223> The 'Xaa' at location 48 stands for Lys, Thr, Met, Glu, Ala,
      Val, Gln, Pro, or Leu.

<220>
<221> misc_feature
<222> (54)..(54)
<223> The 'Xaa' at location 54 stands for Val.
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<220>
<221> misc_feature
<222> (56)..(56)
<223> The 'Xaa' at location 56 stands for Lys, Glu, or Gln.

<220>
<221> misc_feature
<222> (65)..(65)
<223> The 'Xaa' at location 65 stands for Glu, Asp, or Val.

<220>
<221> misc_feature
<222> (66)..(66)
<223> The 'Xaa' at location 66 stands for Ile, Val, or Leu.

<220>
<221> misc_feature
<222> (76)..(76)
<223> The 'Xaa' at location 76 stands for Gly.

<220>
<221> misc_feature
<222> (87)..(87)
<223> The 'Xaa' at location 87 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (93)..(93)
<223> The 'Xaa' at location 93 stands for Asp, or Ala.

<220>
<221> misc_feature
<222> (102)..(102)
<223> The 'Xaa' at location 102 stands for Lys, or Asn.

<220>
<221> misc_feature
<222> (103)..(103)
<223> The 'Xaa' at location 103 stands for Arg, or Ser.

<220>
<221> misc_feature
<222> (109)..(109)
<223> The 'Xaa' at location 109 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (112)..(112)
<223> The 'Xaa' at location 112 stands for Asp, His, or Tyr.

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<221> misc_feature
<222> (114)..(114)
<223> The 'Xaa' at location 114 stands for Arg, or Ser.

<220>
<221> misc_feature
<222> (117)..(117)
<223> The 'Xaa' at location 117 stands for Gly.

<220>
<221> misc_feature
<222> (148)..(148)
<223> The 'Xaa' at location 148 stands for Val.

<220>
<221> misc_feature
<222> (150)..(150)
<223> The 'Xaa' at location 150 stands for Pro.

<220>
<221> misc_feature
<222> (153)..(153)
<223> The 'Xaa' at location 153 stands for Ile, Val, or Phe.

<220>
<221> misc_feature
<222> (154)..(154)
<223> The 'Xaa' at location 154 stands for Glu, or Asp.

<220>
<221> misc_feature
<222> (157)..(157)
<223> The 'Xaa' at location 157 stands for Ser, Gly, or Arg.

<220>
<221> misc_feature
<222> (159)..(159)
<223> The 'Xaa' at location 159 stands for Gly.

<220>
<221> misc_feature
<222> (183)..(183)
<223> The 'Xaa' at location 183 stands for Thr.

<220>
<221> misc_feature
<222> (223)..(223)
<223> The 'Xaa' at location 223 stands for Pro.

<220>
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<221> misc_feature
<222> (225)..(225)
<223> The 'Xaa' at location 225 stands for Ser.

<220>
<221> misc_feature
<222> (237)..(237)
<223> The 'Xaa' at location 237 stands for Ser, Thr, Ile, Gly, Ala,
Val,
      Cys, or Phe.

<220>
<221> misc_feature
<222> (239)..(239)
<223> The 'Xaa' at location 239 stands for Val.

<220>
<221> misc_feature
<222> (241)..(241)
<223> The 'Xaa' at location 241 stands for Val.

<220>
<221> misc_feature
<222> (242)..(242)
<223> The 'Xaa' at location 242 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (246)..(246)
<223> The 'Xaa' at location 246 stands for Lys, Asn, or Thr.

<220>
<221> misc_feature
<222> (251)..(251)
<223> The 'Xaa' at location 251 stands for Tyr, Ser, or Phe.

<220>
<221> misc_feature
<222> (259)..(259)
<223> The 'Xaa' at location 259 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (305)..(305)
<223> The 'Xaa' at location 305 stands for Leu.

<220>
<221> misc_feature
<222> (319)..(319)
<223> The 'Xaa' at location 319 stands for Pro.
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<220>
<221> misc_feature
<222> (346)..(346)
<223> The 'Xaa' at location 346 stands for Lys, Arg, Thr, Gln, Pro, a
      stop codon, Trp, or Ser.

<220>
<221> misc_feature
<222> (411)..(411)
<223> The 'Xaa' at location 411 stands for Lys, Thr, or Met.

<220>
<221> misc_feature
<222> (421)..(421)
<223> The 'Xaa' at location 421 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (457)..(457)
<223> The 'Xaa' at location 457 stands for Leu.

<220>
<221> misc_feature
<222> (458)..(458)
<223> The 'Xaa' at location 458 stands for Pro.

<220>
<221> misc_feature
<222> (466)..(466)
<223> The 'Xaa' at location 466 stands for Pro.

<220>
<221> misc_feature
<222> (487)..(487)
<223> The 'Xaa' at location 487 stands for Gly.

<220>
<221> misc_feature
<222> (493)..(493)
<223> The 'Xaa' at location 493 stands for Val.

<220>
<221> misc_feature
<222> (518)..(518)
<223> The 'Xaa' at location 518 stands for Thr.

<220>
<221> misc_feature
<222> (536)..(536)
<223> The 'Xaa' at location 536 stands for Val.
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<220>
<221> misc_feature
<222> (556)..(556)
<223> The 'Xaa' at location 556 stands for Met, Ile, Val, or Leu.

<220>
<221> misc_feature
<222> (557)..(557)
<223> The 'Xaa' at location 557 stands for Ile, Val, or Leu.

<220>
<221> misc_feature
<222> (558)..(558)
<223> The 'Xaa' at location 558 stands for Thr, Ala, or Pro.

<220>
<221> misc_feature
<222> (559)..(559)
<223> The 'Xaa' at location 559 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (561)..(561)
<223> The 'Xaa' at location 561 stands for Ile, Leu, or Phe.

<220>
<221> misc_feature
<222> (562)..(562)
<223> The 'Xaa' at location 562 stands for Lys, Glu, or Gln.

<220>
<221> misc_feature
<222> (567)..(567)
<223> The 'Xaa' at location 567 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (572)..(572)
<223> The 'Xaa' at location 572 stands for Asn, or Tyr.

<220>
<221> misc_feature
<222> (575)..(575)
<223> The 'Xaa' at location 575 stands for Glu, Ala, or Val.

<220>
<221> misc_feature
<222> (581)..(581)
<223> The 'Xaa' at location 581 stands for Thr, Ala, or Ser.

<220>
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<221> misc_feature
<222> (583)..(583)
<223> The 'Xaa' at location 583 stands for Asn, Asp, or Tyr.

<220>
<221> misc_feature
<222> (617)..(617)
<223> The 'Xaa' at location 617 stands for Pro.

<220>
<221> misc_feature
<222> (618)..(618)
<223> The 'Xaa' at location 618 stands for Pro, or Ser.

<220>
<221> misc_feature
<222> (643)..(643)
<223> The 'Xaa' at location 643 stands for Glu, Asp, Gln, His, a stop
codon, or Tyr.

<220>
<221> misc_feature
<222> (647)..(647)
<223> The 'Xaa' at location 647 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (650)..(650)
<223> The 'Xaa' at location 650 stands for Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> (660)..(660)
<223> The 'Xaa' at location 660 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (708)..(708)
<223> The 'Xaa' at location 708 stands for Asn, Ser, Thr, Asp, Gly,
Ala, Tyr, or Cys.

<220>
<221> misc_feature
<222> (710)..(710)
<223> The 'Xaa' at location 710 stands for Ser, Arg, or Cys.

<400> 30
Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1           5           10          15
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Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
20 25 30

Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
35 40 45

Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp
50 55 60

Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly
65 70 75 80

Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile
85 90 95

Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa
100 105 110

Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu
210 215 220

Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His
225 230 235 240

Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile
245 250 255

Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu
260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala
275 280 285

Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe
305 310 315 320

Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg
325 330 335

Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu
340 345 350

Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp
370 375 380

Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr
385 390 395 400

Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly
405 410 415

Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu
420 425 430

Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met
435 440 445

Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu
450 455 460

Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala
465 470 475 480

Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His
485 490 495

Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu
545 550 555 560

Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp
565 570 575

Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser
645 650 655

Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
675 680 685

Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
690 695 700

Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720